

1642

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/068,377C

DATE: 10/26/2001

TIME: 13:00:04

Input Set : A:\GENENT061CP2seqlist.txt

Output Set: N:\CRF3\10262001\I068377C.raw

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NOV 09 2001

NOV 26 2001

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3 <110> APPLICANT: Lasky, Laurence A.
 4 Dowbenko, Donald J.
 6 <120> TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage Furrow-Associated
 7 Proteins (PSTPIPs)
 9 <130> FILE REFERENCE: P1066P2
 11 <140> CURRENT APPLICATION NUMBER: US 09/068,377C
 12 <141> CURRENT FILING DATE: 1998-05-08
 14 <150> PRIOR APPLICATION NUMBER: PCT/US98/01774
 15 <151> PRIOR FILING DATE: 1998-01-30
 17 <150> PRIOR APPLICATION NUMBER: US 08/938,830
 18 <151> PRIOR FILING DATE: 1997-09-29
 20 <150> PRIOR APPLICATION NUMBER: US 60/104,589
 21 <151> PRIOR FILING DATE: 1997-02-07
 23 <160> NUMBER OF SEQ ID NOS: 73
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 415
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Mus Musculus
 30 <400> SEQUENCE: 1
 31 Met Met Ala Gln Leu Gln Phe Arg Asp Ala Phe Trp Cys Arg Asp
 32 1 5 10 15
 34 Phe Thr Ala His Thr Gly Tyr Glu Val Leu Leu Gln Arg Leu Leu
 35 20 25 30
 37 Asp Gly Arg Lys Met Cys Lys Asp Val Glu Glu Leu Leu Arg Gln
 38 35 40 45
 40 Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile
 41 50 55 60
 43 Ala Arg Lys Ala Gly Gly Gln Thr Glu Met Asn Ser Leu Arg Thr
 44 65 70 75
 46 Ser Phe Asp Ser Leu Lys Gln Gln Thr Glu Asn Val Gly Ser Ala
 47 80 85 90
 49 His Ile Gln Leu Ala Leu Ala Leu Arg Glu Glu Leu Arg Ser Leu
 50 95 100 105
 52 Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Tyr Glu
 53 110 115 120
 55 Ala Ile Met Asp Arg Val Gln Lys Ser Lys Leu Ser Leu Tyr Lys
 56 125 130 135
 58 Lys Thr Met Glu Ser Lys Lys Ala Tyr Asp Gln Lys Cys Arg Asp
 59 140 145 150
 61 Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg Val Ser Ala Asn Gly
 62 155 160 165
 64 His Gln Lys Gln Val Glu Lys Ser Gln Asn Lys Ala Lys Gln Cys
 65 170 175 180
 67 Lys Glu Ser Ala Thr Glu Ala Glu Arg Val Tyr Arg Gln Asn Ile
 68 185 190 195
 70 Glu Gln Leu Glu Arg Ala Arg Thr Glu Trp Glu Gln Glu His Arg
 71 200 205 210

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```

73 Thr Thr Cys Glu Ala Phe Gln Leu Gln Glu Phe Asp Arg Leu Thr
74                215                220                225
76 Ile Leu Arg Asn Ala Leu Trp Val His Cys Asn Gln Leu Ser Met
77                230                235                240
79 Gln Cys Val Lys Asp Asp Glu Leu Tyr Glu Glu Val Arg Leu Thr
80                245                250                255
82 Leu Glu Gly Cys Asp Val Glu Gly Asp Ile Asn Gly Phe Ile Gln
83                260                265                270
85 Ser Lys Ser Thr Gly Arg Glu Pro Pro Ala Pro Val Pro Tyr Gln
86                275                280                285
88 Asn Tyr Tyr Asp Arg Glu Val Thr Pro Leu Ile Gly Ser Pro Ser
89                290                295                300
91 Ile Gln Pro Ser Cys Gly Val Ile Lys Arg Phe Ser Gly Leu Leu
92                305                310                315
94 His Gly Ser Pro Lys Thr Thr Pro Ser Ala Pro Ala Ala Ser Thr
95                320                325                330
97 Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu Leu Val Tyr Ala
98                335                340                345
100 Ser Ile Glu Val Gln Ala Thr Gln Gly Asn Leu Asn Ser Ser Ala
101                350                355                360
103 Gln Asp Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp
104                365                370                375
106 Glu Leu Asp Ile Ser Ala Gly Asp Ile Leu Ala Val Ile Leu Glu
107                380                385                390
109 Gly Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg Gly
110                395                400                405
112 Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu
113                410                415
115 <210> SEQ ID NO: 2
116 <211> LENGTH: 2100
117 <212> TYPE: DNA
118 <213> ORGANISM: Mus Musculus
120 <400> SEQUENCE: 2
121 caatatattca agctatacca agcatataat caactccaag cttatgccca 50
123 agaagaagcg gaagggtctcg agcgggcgcca attttaatca aagtgggaat 100
125 attgctgata gctcattgtc cttcactttc actaacagta gcaacggtcc 150
127 gaacctcata acaactcaaa caaattctca agcgctttca caaccaattg 200
129 cctcctctaa cgttcatgat aacttcatga ataatgaaat cacggctagt 250
131 aaaattgatg atggtaataa ttcaaaaacca ctgtcacctg gttggacgga 300
133 ccaaactgcg tataacgcgt ttggaatcac tacagggatg tttaatacca 350
135 ctacaatgga tgatgtatat aactatctat tcgatgatga agatacccca 400
137 ccaaaccocaa aaaaagaggg tgggtcgacc cacgcgtccg gtccttcct 450
139 catttgcgtg ctgattctag ccccaaacaa aacagggttg gcctttttcc 500
141 tcctccggca gttgcctctg gcttgtggct gccttctgag cgtttcagac 550
143 ggcgcgggct gggagtgagg gggagggcct gggctagccg cgctgggact 600
145 gggacgtgct cctggctcct ggcccatgct cagccctgct tgaagcagga 650
147 gtgctagcat ttgacacaac gcccttggag gatgatggcc cagctgcagt 700
149 tccgagatgc cttctggtgc agggacttca cggccacac agggtatgag 750
151 gtgctactgc agaggctgct ggacggcagg aagatgtgca aggatgtgga 800

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153 ggagctgctc agacagaggg cccaggcgga ggagaggtag gggaaggagc 850
155 tgggtgcagat tgcacgcaag gctgggtggc agacagagat gaattccctg 900
157 aggacctcct ttgactccct gaagcagcaa acagagaatg tgggcagtgc 950
159 acacatccag ctggccctgg cctgcgtga ggagctgcgg agcctggagg 1000
161 agttccgaga gagacagaaa gagcagcgga agaagtatga ggccatcatg 1050
163 gaccgtgtcc agaagagcaa gttgtcgctc tacaagaaga ccatggagtc 1100
165 caagaaggca tatgaccaga agtgcaggga tgcagatgat gctgagcagg 1150
167 ccttcgagcg tgtgagtgcc aatggccacc agaagcaagt agaaaagagc 1200
169 cagaacaaaag ccaagcagtg caaggagtca gccacagagg cagaaagagt 1250
171 gtacaggcaa aatatcgaac aactggagag agcgaggacc gagtgggagc 1300
173 aggagcaccg gactacctgt gaggccttcc agttgcagga gtttgaccgg 1350
175 ctcaccatcc tccgcaatgc cctgtgggtg cactgtaacc agctctccat 1400
177 gcagtgtgtc aaggatgatg agctctatga ggaagtgcgg ctgacccttg 1450
179 agggctgtga tgtggaaggt gacatcaatg gcttcatcca gtccaagagc 1500
181 actggcagag agccccagc tccggtgcct tatcagaact actatgacag 1550
183 ggaggtgacc ccactgattg gcagccctag catccagccc tcctgcggtg 1600
185 tgataaagag gttctctggg ctgctacatg gaagtcccaa gaccacacct 1650
187 tctgtccttg ctgcttccac agagactctg actcccaccc ctgagcggaa 1700
189 tgagttggtc tacgcatcca tcgaagtgca ggcgaccagc ggaaacctta 1750
191 actcatcagc ccaggactac cgggcactct acgactacac tgcacagaat 1800
193 tctgatgagc tggacatttc cgcgggagac atcctggcgg tcctcctgga 1850
195 aggggaggat ggctggtgga ctgtggagcg gaacggacaa cgtggctttg 1900
197 tccctgggtc gtacttggag aagctctgag gaaaggctag cagtctccac 1950
199 atacctccgc cctgactgtg aggtcaggac tgtttctttc catcaccgcc 2000
201 caggcctcac ggggccagaa ccaagcccgg tgggtgctgg catgggctgg 2050
203 gtgctggcta ctctcaataa atgtctccca gaaggaaaaa aaaaaaaaaa 2100

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205 <210> SEQ ID NO: 3

206 <211> LENGTH: 48

207 <212> TYPE: PRT

208 <213> ORGANISM: Mus Musculus

210 <400> SEQUENCE: 3

```

211 Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp Glu Leu Asp Ile Ser
212 1 5 10 15
214 Ala Gly Asp Ile Leu Ala Val Ile Leu Glu Gly Glu Asp Gly Trp
215 20 25 30
217 Trp Thr Val Glu Arg Asn Gly Gln Arg Gly Phe Val Pro Gly Ser
218 35 40 45

```

220 Tyr Leu Arg

223 <210> SEQ ID NO: 4

224 <211> LENGTH: 50

225 <212> TYPE: PRT

226 <213> ORGANISM: Homo sapien

228 <400> SEQUENCE: 4

```

229 Leu Tyr Gln Tyr Ile Gly Gln Asp Val Asp Glu Leu Ser Phe Asn
230 1 5 10 15
232 Val Asn Glu Val Ile Glu Ile Leu Ile Glu Asp Ser Ser Gly Trp
233 20 25 30
235 Trp Lys Gly Arg Leu His Gly Gln Glu Gly Leu Phe Pro Gly Asn
236 35 40 45

```

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```

238 Tyr Val Glu Lys Ile
239                      50
241 <210> SEQ ID NO: 5
242 <211> LENGTH: 50
243 <212> TYPE: PRT
244 <213> ORGANISM: Homo sapien
246 <400> SEQUENCE: 5
247 Leu Tyr Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys
248   1                      5                      10                      15
250 Lys Gly Asp Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp
251                      20                      25                      30
253 Trp Lys Val Glu Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala
254                      35                      40                      45
256 Tyr Val Lys Lys Leu
257                      50
259 <210> SEQ ID NO: 6
260 <211> LENGTH: 50
261 <212> TYPE: PRT
262 <213> ORGANISM: Homo sapien
264 <400> SEQUENCE: 6
265 Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser Phe Asp
266   1                      5                      10                      15
268 Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu Gly Trp
269                      20                      25                      30
271 Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala Asn
272                      35                      40                      45
274 Tyr Val Lys Leu Leu
275                      50
277 <210> SEQ ID NO: 7
278 <211> LENGTH: 48
279 <212> TYPE: PRT
280 <213> ORGANISM: Homo sapien
282 <400> SEQUENCE: 7
283 Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser Phe Asp
284   1                      5                      10                      15
286 Pro Asp Asp Ile Ile Thr Asn Ile Glu Met Ile Asp Asp Gly Trp
287                      20                      25                      30
289 Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn
290                      35                      40                      45
292 Tyr Val Glu
295 <210> SEQ ID NO: 8
296 <211> LENGTH: 8
297 <212> TYPE: PRT
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Amino acid epitope tag
303 <400> SEQUENCE: 8
304 Asp Tyr Lys Asp Asp Asp Lys
305   1                      5

```

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Input Set : A:\GENENT061CP2seqlist.txt

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307 <210> SEQ ID NO: 9
308 <211> LENGTH: 33
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
315 <400> SEQUENCE: 9
316 cgcggatcca ccatgatggc ccagctgcag ttc 33
318 <210> SEQ ID NO: 10
319 <211> LENGTH: 45
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
326 <400> SEQUENCE: 10
327 gtacgcgtcg actcacttgt catcgctcgtc cttgtagtcg agctt 45
329 <210> SEQ ID NO: 11
330 <211> LENGTH: 18
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
337 <400> SEQUENCE: 11
338 tgcctttctc tccacagg 18
340 <210> SEQ ID NO: 12
341 <211> LENGTH: 36
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
345 <220> FEATURE:
346 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
348 <400> SEQUENCE: 12
349 ctccttgagg ttctactagt gggggctggt gtcctg 36
351 <210> SEQ ID NO: 13
352 <211> LENGTH: 39
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial Sequence
356 <220> FEATURE:
357 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
359 <400> SEQUENCE: 13
360 gcggcgcac tagtatccag tctgtgctcc atctgttac 39
362 <210> SEQ ID NO: 14
363 <211> LENGTH: 17
364 <212> TYPE: DNA
365 <213> ORGANISM: Artificial Sequence
367 <220> FEATURE:
368 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
370 <400> SEQUENCE: 14
371 gcgtttggaa tcactac 17
373 <210> SEQ ID NO: 15

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27